

SEQUENCE LISTING

<110> Ruelle, Jean-Louis

<120> Novel Compounds

<130> BM45332

<150> PCT/EP99/06781

<151> 1999-09-14

<150> GB 9820002.5

<151> 1998-09-14

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<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1329

<212> DNA

<213> Moraxella catarrhalis

<400> 1

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<210> 2

<211> 442

<212> PRT

<213> Moraxella catarrhalis

<400> 2

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Met Lys Val Ser Leu Ser Thr Leu Thr Leu Ser Ile Leu Ser Cys Phe
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Ala Ile Leu Ala Ile Gln Gln Ala Gln Ala Val Pro Asn Pro Val Ala
          20          25          30
Phe Val Asp Glu Val Arg Ser Glu Asn Asp Leu Gly Gln Asp Asn Glu
      35              40              45

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Leu Pro Ile Asp Val Gln Ser Ala Thr Gln Ser Ala Ser Thr Asp Thr
 50 55 60
 Ala Asn Pro Leu Asp Glu His Glu Pro Glu Leu Tyr Thr Thr Ala Leu
 65 70 75 80
 Glu Asn Lys Thr Met Leu Ile Asn Cys Ser Ala Leu Asn Gln Asp Ile
 85 90 95
 Met Arg Leu Ala Cys Tyr Asp Thr Leu Val His Gly Glu Thr Pro Ala
 100 105 110
 Val Ile Lys Thr Lys Arg Ser Ile Arg Leu Asp Glu Thr Ile Trp Gln
 115 120 125
 Thr Ile Lys Gly Lys Pro Gln Val Ile Tyr Gln Glu Thr Thr Asp Pro
 130 135 140
 Ile Phe Leu Met Gly Asn Glu Lys Gly Met Leu Thr Lys Lys Asp Ala
 145 150 155 160
 Lys Gln Leu Glu Tyr Ala Ala Lys Gln Phe Thr Pro Leu Ser Leu Ser
 165 170 175
 Phe Asp Leu Asp Arg Asn Asn Thr Pro Leu Trp Ser Ser Arg Pro His
 180 185 190
 Asn Pro Met Tyr Val Leu Pro Ile Phe Met His Gly Lys Pro Asn Arg
 195 200 205
 Ser Pro Asn Thr Pro Ser His Glu Ala Lys Gln Phe Thr Pro Asn Glu
 210 215 220
 Phe Arg Ala Pro Glu Leu Lys Phe Gln Val Ser Val Lys Val Lys Ala
 225 230 235 240
 Ala Glu Asp Leu Trp Gly Thr Asp Ser Asp Leu Trp Phe Gly Tyr Thr
 245 250 255
 Gln Gln Ser His Trp Gln Ile Phe Asn Gly Lys Asn Ser Arg Pro Phe
 260 265 270
 Arg Val His Asp Tyr Gln Pro Glu Ile Phe Leu Thr Gln Pro Val Tyr
 275 280 285
 Ser Asp Leu Pro Trp Asp Gly Lys Val Arg Met Ile Gly Met Gly Ala
 290 295 300
 Val His His Ser Asn Gly Glu Ser Ala Lys Leu Ser Arg Ser Trp Asn
 305 310 315 320
 Arg Ala Tyr Leu Met Ala Gly Met Glu Trp Lys Asn Leu Thr Val Met
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 Pro Arg Ile Trp Gly Arg Ile Phe Lys Glu Gly Ser Gly Ser Gln Pro
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 Asp Asp Asn Pro Asp Ile Leu Asp Tyr Tyr Gly Tyr Gly Asp Val Arg
 355 360 365
 Phe Leu Tyr Gln Leu Glu Asn Lys Ser Asn Ile Ser Gly Thr Val Arg
 370 375 380
 Tyr Asn Pro Arg Ser Gly Lys Gly Ala Leu Gln Leu Asp Tyr Val Tyr
 385 390 395 400
 Pro Leu Gly Lys Gly Ile Ser Gly Tyr Phe Gln Ile Phe Gln Gly Tyr
 405 410 415
 Gly Gln Ser Leu Ile Asp Tyr Asn His Glu Ala Thr Ser Phe Gly Val
 420 425 430
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<210> 3

<211> 1329

<212> DNA

<213> Moraxella catarrhalis

<400> 3

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aatgatcttg	ggcaagacaa	tgaattactc	attggtgtac	aaagtgcgac	acaatcagcg	180
tctactgata	cggtaatcc	tttagacgaa	catgaaccag	agctttatac	gacagcttta	240
gaaaataaaa	ccatgctgat	taactgctca	gcacttaatc	aagatatcat	gcgtttggcg	300

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acgacagatc cgattttttt aatgggtaat gaaaaaggca tgctgaccaa aaaagatgcc 480
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cgaaataata caccgctttg gtcatcacga ccacacaatc cgatgtatgt attgcccata 600
tttatgcacg gtaagcctaa tcgaagccca aatacgccca gtcatgaagc aagacaattt 660
accccaaattg aatttcgtgc ccctgaatta aaatttcaag tttctgttaa ggtaaagct 720
gctgaggatt tatgggggac ggattcagat ttatggtttg ggtatacaca gcaatcgcac 780
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<210> 4
<211> 442
<212> PRT
<213> Moraxella catarrhalis

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<400> 4
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Phe Val Asp Glu Val Arg Ser Lys Asn Asp Leu Gly Gln Asp Asn Glu
35 40 45
Leu Leu Ile Gly Val Gln Ser Ala Thr Gln Ser Ala Ser Thr Asp Thr
50 55 60
Ala Asn Pro Leu Asp Glu His Glu Pro Glu Leu Tyr Thr Thr Ala Leu
65 70 75 80
Glu Asn Lys Thr Met Leu Ile Asn Cys Ser Ala Leu Asn Gln Asp Ile
85 90 95
Met Arg Leu Ala Cys Tyr Asp Thr Leu Val His Gly Glu Thr Pro Ala
100 105 110
Val Ile Lys Thr Lys Arg Ser Ile Arg Leu Asp Glu Thr Ile Trp Gln
115 120 125
Thr Ile Lys Gly Lys Pro Gln Val Val Tyr Gln Glu Thr Thr Asp Pro
130 135 140
Ile Phe Leu Met Gly Asn Glu Lys Gly Met Leu Thr Lys Lys Asp Ala
145 150 155 160
Lys Gln Leu Glu Tyr Ala Ala Lys Gln Phe Thr Pro Leu Ser Leu Ser
165 170 175
Phe Asp Leu Asp Arg Asn Asn Thr Pro Leu Trp Ser Ser Arg Pro His
180 185 190
Asn Pro Met Tyr Val Leu Pro Ile Phe Met His Gly Lys Pro Asn Arg
195 200 205
Ser Pro Asn Thr Pro Ser His Glu Ala Arg Gln Phe Thr Pro Asn Glu
210 215 220
Phe Arg Ala Pro Glu Leu Lys Phe Gln Val Ser Val Lys Val Lys Ala
225 230 235 240
Ala Glu Asp Leu Trp Gly Thr Asp Ser Asp Leu Trp Phe Gly Tyr Thr
245 250 255
Gln Gln Ser His Trp Gln Ile Phe Asn Gly Lys Asn Ser Arg Pro Phe
260 265 270
Arg Val His Asp Tyr Gln Pro Glu Ile Phe Leu Thr Gln Pro Val Tyr
275 280 285
Ser Asp Leu Pro Trp Asp Gly Lys Val Arg Met Ile Gly Met Gly Ala

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      290      295      300
Val His His Ser Asn Gly Glu Ser Ala Lys Leu Ser Arg Ser Trp Asn
305      310      315      320
Arg Ala Tyr Leu Met Ala Gly Met Glu Trp Lys Asn Leu Thr Val Met
      325      330      335
Pro Arg Ile Trp Gly Arg Ile Phe Lys Glu Gly Ser Gly Ser Gln Pro
      340      345      350
Asp Asp Asn Pro Asp Ile Leu Asp Tyr Tyr Gly Tyr Gly Asp Val Arg
      355      360      365
Phe Leu Tyr Gln Leu Glu Asn Lys Ser Asn Ile Ser Gly Thr Val Arg
      370      375      380
Tyr Asn Pro Arg Ser Gly Lys Gly Ala Leu Gln Leu Asp Tyr Val Tyr
385      390      395      400
Pro Leu Gly Lys Gly Ile Ser Gly Tyr Phe Gln Ile Phe Gln Gly Tyr
      405      410      415
Gly Gln Ser Leu Ile Asp Tyr Asn His Glu Ala Thr Ser Phe Gly Val
      420      425      430
Gly Leu Met Leu Asn Asp Trp Met Gly Leu
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<210> 5
<211> 1329
<212> DNA
<213> Moraxella catarrhalis

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tctactgata cggctaatacc tttagacgaa catgaaccag agctttatac gacagcttta      240
gaaaataaaa ccattgctgat taactgctca gcacttaatc aagatatcat gcgtttggcg      300
tgctatgaca ctttggtgca tggtagagac ccagcggtaa ttaaaaccaa gcgttcatt      360
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cgaaataata caccactttg gtcatcacga ccacacaatc cgatgtatgt attgcccata      600
tttatgcacg gtaagcctaa tcgaagccca aatacgccca gtcatgaagc aagacaattt      660
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gctgaggatt tatgggggac ggattcagat ttatggtttg gatatacaca gcaatcgac      780
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ggtctataa      1329

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<210> 6
<211> 442
<212> PRT
<213> Moraxella catarrhalis

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<400> 6
Met Lys Val Ser Leu Ser Thr Leu Thr Leu Ser Ile Leu Ser Cys Phe
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Ala Ile Leu Ala Ile Gln Gln Ala Lys Ala Val Pro Asn Pro Val Ala
20      25      30
Phe Val Asp Glu Val Arg Ser Glu Asn Asp Leu Gly Gln Asp Asn Glu
35      40      45

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Leu Pro Ile Asp Val Gln Ser Ala Thr Gln Ser Ala Ser Thr Asp Thr
 50 55 60
 Ala Asn Pro Leu Asp Glu His Glu Pro Glu Leu Tyr Thr Thr Ala Leu
 65 70 75 80
 Glu Asn Lys Thr Met Leu Ile Asn Cys Ser Ala Leu Asn Gln Asp Ile
 85 90 95
 Met Arg Leu Ala Cys Tyr Asp Thr Leu Val His Gly Glu Thr Pro Ala
 100 105 110
 Val Ile Lys Thr Lys Arg Ser Ile Arg Leu Asp Glu Thr Ile Trp Gln
 115 120 125
 Thr Ile Lys Gly Lys Pro Gln Val Val Tyr Gln Glu Thr Thr Asp Pro
 130 135 140
 Ile Phe Leu Met Gly Asn Glu Lys Gly Met Leu Thr Lys Lys Asp Ala
 145 150 155 160
 Lys Gln Leu Glu Tyr Ala Ala Lys Gln Phe Thr Pro Leu Ser Leu Ser
 165 170 175
 Phe Asp Leu Asp Arg Asn Asn Thr Pro Leu Trp Ser Ser Arg Pro His
 180 185 190
 Asn Pro Met Tyr Val Leu Pro Ile Phe Met His Gly Lys Pro Asn Arg
 195 200 205
 Ser Pro Asn Thr Pro Ser His Glu Ala Arg Gln Phe Thr Pro Asn Glu
 210 215 220
 Phe Arg Ala Pro Glu Leu Lys Phe Gln Val Ser Val Lys Val Lys Ala
 225 230 235 240
 Ala Glu Asp Leu Trp Gly Thr Asp Ser Asp Leu Trp Phe Gly Tyr Thr
 245 250 255
 Gln Gln Ser His Trp Gln Ile Phe Asn Gly Lys Asn Ser Arg Pro Phe
 260 265 270
 Arg Val His Asp Tyr Gln Pro Glu Ile Phe Leu Thr Gln Pro Val Tyr
 275 280 285
 Ser Asp Leu Pro Trp Asp Gly Lys Val Arg Met Ile Gly Met Gly Ala
 290 295 300
 Val His His Ser Asn Gly Glu Ser Ala Lys Leu Ser Arg Ser Trp Asn
 305 310 315 320
 Arg Ala Tyr Leu Met Ala Gly Met Glu Trp Lys Asn Leu Thr Val Met
 325 330 335
 Pro Arg Ile Trp Gly Arg Ile Phe Lys Glu Gly Ser Gly Ser Gln Pro
 340 345 350
 Asp Asp Asn Pro Asp Ile Leu Asp Tyr Tyr Gly Tyr Gly Asp Val Arg
 355 360 365
 Phe Leu Tyr Gln Leu Glu Asn Lys Ser Asn Ile Ser Gly Thr Val Arg
 370 375 380
 Tyr Asn Pro Arg Ser Gly Lys Gly Ala Leu Gln Leu Asp Tyr Val Tyr
 385 390 395 400
 Pro Leu Gly Lys Gly Ile Ser Gly Tyr Phe Gln Ile Phe Gln Gly Tyr
 405 410 415
 Gly Gln Ser Leu Ile Asp Tyr Asn His Glu Ala Thr Ser Phe Gly Val
 420 425 430
 Gly Leu Met Leu Asn Asp Trp Met Gly Leu
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<210> 7

<211> 1329

<212> DNA

<213> Moraxella catarrhalis

<400> 7

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aatgatcttg	ggcaagacaa	tgaattaccc	attgatgtcc	aaagtgcgac	acaatcggcg	180
tctactgata	cggtaatcc	tttagacgaa	catgaaccag	agctttatac	gacagcttta	240
gaaaataaaa	ccatgtctgat	taactgctca	gcacttaatc	aagatatcat	gcgtttggcg	300

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cgccttgatg aaacaatttg gcagaccatc aaaggcaaac cccaggttgt ctatcaagaa 420
acgacagatc cgattttttt aatgggtaat gaaaaaggca tgctgaccaa aaaagatgcc 480
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tggcagattt ttaatggaaa aaactctcgt ccttttagag tacatgacta ccagccagag 840
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<210> 8

<211> 442

<212> PRT

<213> Moraxella catarrhalis

<400> 8

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Met Lys Val Ser Leu Ser Thr Leu Thr Leu Ser Ile Leu Pro Cys Phe
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Ala Ile Leu Ala Ile Gln Gln Ala Gln Ala Val Pro Asn Pro Val Ala
 20          25          30
Phe Val Asp Glu Val Arg Ser Glu Asn Asp Leu Gly Gln Asp Asn Glu
 35          40          45
Leu Pro Ile Asp Val Gln Ser Ala Thr Gln Ser Ala Ser Thr Asp Thr
 50          55          60
Ala Asn Pro Leu Asp Glu His Glu Pro Glu Leu Tyr Thr Thr Ala Leu
 65          70          75          80
Glu Asn Lys Thr Met Leu Ile Asn Cys Ser Ala Leu Asn Gln Asp Ile
 85          90          95
Met Arg Leu Ala Cys Tyr Asp Thr Leu Val His Gly Glu Thr Pro Ala
100          105          110
Val Ile Lys Thr Lys Arg Ser Ile Arg Leu Asp Glu Thr Ile Trp Gln
115          120          125
Thr Ile Lys Gly Lys Pro Gln Val Val Tyr Gln Glu Thr Thr Asp Pro
130          135          140
Ile Phe Leu Met Gly Asn Glu Lys Gly Met Leu Thr Lys Lys Asp Ala
145          150          155          160
Lys Gln Leu Glu Tyr Ala Ala Lys Gln Phe Thr Pro Leu Ser Leu Ser
165          170          175
Phe Asp Leu Asp Arg Asn Asn Thr Pro Leu Trp Ser Ser Arg Pro His
180          185          190
Asn Pro Met Tyr Val Leu Pro Ile Phe Met His Gly Lys Pro Asn Arg
195          200          205
Ser Pro Asn Thr Pro Ser His Glu Ala Lys Gln Phe Thr Pro Asn Glu
210          215          220
Phe Arg Ala Pro Glu Leu Lys Phe Gln Val Ser Val Lys Val Lys Ala
225          230          235          240
Ala Glu Asp Leu Trp Gly Thr Asp Ser Asp Leu Trp Phe Gly Tyr Thr
245          250          255
Gln Gln Ser His Trp Gln Ile Phe Asn Gly Lys Asn Ser Arg Pro Phe
260          265          270
Arg Val His Asp Tyr Gln Pro Glu Ile Phe Leu Thr Gln Pro Val Tyr
275          280          285
Ser Asp Leu Pro Trp Asp Gly Lys Val Arg Met Ile Gly Met Gly Ala

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      290              295              300
Val His His Ser Asn Gly Glu Ser Ala Lys Leu Ser Arg Ser Trp Asn
305              310              315              320
Arg Ala Tyr Leu Met Ala Gly Met Glu Trp Lys Asn Leu Thr Val Met
              325              330              335
Pro Arg Ile Trp Gly Arg Ile Phe Lys Glu Gly Ser Gly Ser Gln Pro
              340              345              350
Asp Asp Asn Pro Asp Ile Leu Asp Tyr Tyr Gly Tyr Gly Asp Val Arg
              355              360              365
Phe Leu Tyr Gln Leu Glu Asn Lys Ser Asn Ile Ser Gly Thr Val Arg
              370              375              380
Tyr Asn Pro Arg Ser Gly Lys Gly Ala Leu Gln Leu Asp Tyr Val Tyr
385              390              395              400
Pro Leu Gly Lys Gly Ile Ser Gly Tyr Phe Gln Ile Phe Gln Gly Tyr
              405              410              415
Gly Gln Ser Leu Ile Asp Tyr Asn His Glu Ala Thr Ser Phe Gly Val
              420              425              430
Gly Leu Met Leu Asn Asp Trp Met Gly Leu
              435              440

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<210> 9
<211> 22
<212> DNA
<213> Artificial Sequence

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<220>
<223> Primer sequence

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<400> 9
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22

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<210> 10
<211> 21
<212> DNA
<213> Artificial Sequence

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<220>
<223> Primer sequence

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<400> 10
gtatgggttg atcaaataca g

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21

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<210> 11
<211> 58
<212> DNA
<213> Artificial Sequence

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<220>
<223> Oligonucleotide

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58

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<210> 12
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<212> DNA
<213> Artificial Sequence

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<220>
<223> Oligonucleotide

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<400> 12

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<210> 13

<211> 1000

<212> DNA

<213> Moraxella catarrhalis

<400> 13

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tcgtaaaaag	cttaccceaag	atccgctttt	gggcttggtg	gcagcggttt	ctgtgggtgt	180
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tttaaagtgtg	gtcatgacgc	aggcaggtgg	gtttattgag	attcaaggca	cagcagaaga	300
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gcagattatc	gaagcccaaa	agcaagtatt	aggctggtga	tatgctaatac	gttgaagata	420
atggcgtgat	catcacatta	aatggacaag	taaaagaccc	attattttgg	tggtcgatga	480
tattgctgct	gctgggtgtc	ttggtggcaa	tcatttggtt	gattgcaccc	gttttttatg	540
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aagccaaaac	ttgtcatatg	ttttcacaag	gtcgcttgaa	gattacgtcc	aaacgctttg	660
agattcataa	caaataccta	accttatcag	catcggcaac	aatatctgct	aaagataaca	720
aaatgacaat	tgttgatcgg	ggcattgaat	atcattttac	aggttttgct	gatgaccgtg	780
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